

**Amendments to the Specification**

Please replace the previous Sequence Listing with the new Sequence Listing submitted herewith.

Please replace Table III beginning on page 40, with the following replacement Table III. Please note that the changes to Table III are shown relative to the Table III as filed.

**TABLE III**  
**Oligonucleotides for Construction of Representative Partial TM Genes**

<u>OLIGO</u>	<u>SEQUENCE</u>
1:	gat cag gaa gat gaa cgt att gtt ctg gtt gac aac aag tgc aag tgt gct cgt att act t
2:	cta gaa gta ata cga gca cac ttg cac ttg ttg tca acc aga aca ata cgt tca tct tcc t
1.1:	gat cag aag tgc aag tgt gct cgt att act t
2.1:	ct aga agt aat acg agc aca ctt gca ctt ct
1.2ser:	gat cag gaa gat gaa cgt att gtt ctg gtt gac aac aag tgc aag tcc gct cgt att act t
2.2ser:	cta gaa gta ata cga gcg gac ttg cac ttg ttg tca acc aga aca ata cgt tca tct tcc t
1.2val:	gat cag gaa gat gaa cgt att gtt ctg gtt gac aac aag tgc aag gtt gct cgt att act t
2.2val:	cta gaa gta ata cga gca acc ttg cac ttg ttg tca acc aga aca ata cgt tca tct tcc t
3:	cta gaa tca tcc gta gct cag agg acc caa atg aag ata tag tgc aa
4	gat acg gat gtt acg ttc gac tat atc ttc att tgg gtc ctc tga gct acg gat gat t
5:	cgt aac atc cgt atc atc gtc cca ctg aat aac cgg gag aat atc tca g
5.1dg:	cgt aac atc cgt atc atc gtc cca ctg aat aac cgg gag cac atc tca g
6:	acg gac ttg tag gat ctg aga tat tct ccc ggt tat tca gtg gga cga t
6.1dg:	acg gac ttg tag gat ctg aga tgt gct ccc ggt tat tca gtg gga cga t
7:	atc cta caa gtc cgt tgc gca cac gct tgc tat acc acc tgt ca
8:	gat ctg aca ggt ggt ata cga agc gtg tgc gca

9: gat ctg tgt aag aag tgt gat cca aca gag gta gag ctg gac aat cag ata  
gtc act gca

9L3A: gat ctg tgt aag aag gat gag gac agc gct aca gaa acc tgc tg

10L3A: aat tca gca ggt ttc tgt agc gct gtc ctc atc ctt ctt aca ca

9L3AKDEL: gat ctg tgt aag aag gat gag gac agc gct aca gaa acc tgc tac gag aag  
gat gag ctg tg

10L3AKDEL: aat tca cag ctc atc ctt cgc gtc gca ggt ttc tgt agc gct gtc ctc  
atc ctt ctt aca ca

9.2A3: gat ctg tgt aag aag tct gat atc gat gaa gat tcc gct aca gaa acc tgc  
agc aca tg

10.2A3: aat tca tgt gct gca ggt ttc tgt agc gga atc ttc atc gat atc aga ctt  
ctt aca ca

9.3A3/ser68: gat ctg tct aag aag tct gat atc gat gaa gat tac aga ttc ttc aga  
cta tag cta ctt cta a

10.3A3/ser68: aat ctt cat cga tat cag act tct tag aca

9.3A3/val68: gat ctg gtt aag aag tct gat atc gat gaa gat tac caa ttc ttc aga  
cta tag cta ctt cta a

10.3A3/val68: aat ctt cat cga tat cag act tct taa cca

10: att gtc cag ctc tac ctc tgt tgg atc aca ctt ctt aca ca

11: act caa agc aac att tgc gat gag gac agc gct aca gaa acc tgc a

12: ggt ttc tgt agc gct ctg ctc atc gca aat gtt gct ttg agt cgc agt gac  
tat ctg

13: gc acc tac gat agg aac aaa tgc tac acg gcc gtg gtt ccg ctc gtg tat  
ggt gga gag

14: gag cgg aac cac ggc cgt gta gca ttt gtt cct atc gta ggt gct gca

15: aca aaa atg gtg gaa act gcc ctt acg ccc gat gca tgc tat ccg gac tg

16: aat tca gtc cgg ata gca tgc atc ggg cgt aag ggc agt ttc cac cat ttt  
tgt ctc tcc acc ata cac

15KDEL: aca aaa atg gtg gaa act gcc ctt acg ccc gat gca tgc tat ccg gac aag  
gat gaa ttg tg

16KDEL: aat tca caa ttc atc ctt gtc cgg ata gca tgc atc ggg cgt aag ggc agt  
ttc cac cat ttt tgt ctc tcc acc ata cac

P1: gat cag gtc gct gcc atc caa gac ccg agg ctg ttc gcc gaa gag aag  
gcc gtc gct gac tcc aag tgc aag tgt gct cgt att act t

P2: ct aga agt aat acg agc aca ctt gca ctt gga gtc agc gac ggc ctt ctc

ttc ggc gaa cag cct cgg gtc ttg gat ggc agc gac ct

Tp1: gc gat gac gac gat aag gcc caa acg gag acc tgt act gtt gcg cct cgt  
gaa cgg caa aac tgc gga ttc ccg ~~gaa~~ gga

Tp2: gtt ttg ccg ttc acg agg cgc aac agt aca ggt ctc cgt ttg ggc ctt atc  
gtc gtc atc gct ~~tea~~ gca

Tp3: gta aca ccc tct cag tgc gct aat aaa ggc tgc tgt ttt gat gac acg gta  
cgg ggc gtt ccg tgg tgc ~~ttc~~

Tp4: gcc ccg tac cgt gtc atc aaa aca gca gcc ttt att agc gca ctg aga ggg  
tgt tac ~~tte~~ tcc cgg gaa tcc gca

Tp5: tac ccc aat aca att gac gtt ccg cct gaa gaa gag tgc gag ~~eeg~~ ttt taa g

Tp6: aattc tta cgg ctc gca ctc ttc ttc agg cgg caa gtc aat tgt att ggg gta  
~~gaa~~ gca cca ~~egg~~ aaa aac

Please replace Table X beginning on page 49, with the following replacement Table X.  
Please note that the changes to Table III are shown relative to the Table III as filed.

Table X  
DNA and Primary Amino Acid Sequence of TpS2

101 102  
cys ser asp asp asp lys ala gln thr glu thr cys thr val ala pro  
gc gat gac gac gat aag gcc caa acg gag acc tgt act gtt gcg cct  
~~aet~~ acg tgc cta ctg ctg cta ttc cgg gtt tgc ctc tgg aca tga caa cgc gga  
arg glu arg gln asn cys gly phe pro gly val thr pro ser gln cys ala  
cgt gaa cgg caa aac tgc gga ttc ccg ~~gaa~~ gga/gta aca ccc tct cag tgc gct  
gca ctt gcc gtt ttg/acg cct aag ggc ~~ett~~ cct cat tgt ggg aga gtc acg cga  
asn lys gly cys cys phe asp asp thr val arg gly val pro trp cys phe  
aat aaa ggc tgc tgt ttt gat gac acg gta cgg ggc gtt ccg tgg tgc ~~ttc~~/  
tta ttt ccg acg aca aaa cta ctg tgc cat gcc ccg/caa ggc acc acg ~~aag~~  
tyr pro asn thr ile asp val pro pro glu glu glu cys glu phe  
tac ccc aat aca att gac gtt ccg cct gaa gaa gag tgc gag ~~eeg~~ ttt taa g  
atg ggg tta tgt taa ctg caa ggc gga ctt ctt ctc acg ctc ~~gge~~ aaa att  
cttaa --

### **Remarks**

A new Sequence Listing paper copy and computer disk are filed herewith to correct informalities in the previously filed Sequence Listing. The specification has been amended herein to correct typographical errors in certain DNA sequences. The new version of Table III amends Tp1 (SEQ ID NO: 87), Tp2 (SEQ ID NO: 88), Tp4 (SEQ ID NO: 90), Tp5 (SEQ ID NO: 91), and Tp6 (SEQ ID NO: 92). Also amended is Table X - Tp2 DNA sequence (SEQ ID NOs. 16 and 36). Basis for the changes is as follows. Please note that all references to nucleotide bases are from 5' to 3'.

In the last base in the first codon of the anti-sense strand of the double stranded DNA sequence shown in Table X was modified from a "t" to "g." This changes the codon from act, the anti-sense of a stop codon, to acg, the anti-sense of the codon tgc which encodes cytseine, the amino acid indicated to be encoded in table X. No new matter is implicated by this change as the anti-sense codon has been conformed to be complementary to the proper codon of the sense strand to encode the amino acid sequence indicated in the table. This change to the anti-sense strand codon relating to the specified cys residue of Table X has also been made to the corresponding codon in the Tp2 sequence seen in Table III (i.e., tca to gca).

The middle base in what is the sense strand for codon 127 encoding gly (within the sequence pro-gly-val) of the double stranded DNA sequence of Table X has been changed from "a" to "g." Thus, the codon gaa has been changed to gga to properly encode the indicated amino acid glycine. Support for the gly residue at position 127 in Table X is found in the specification at page 37, paragraph [0115] (citing to Suemeri et al., PNAS 88:11017-11021, 1991 for the sequence of TpS2) and by Suemeri et al., Fig. 3 (copy previously attached), which shows a gly in the same position for TpS2. No new matter is implicated by this change as the encoding DNA sequence has been conformed to the amino acid sequence of the table. The anti-sense strand codon that corresponds to this change also has been changed from ctt to cct. No new matter is added as this change is predicted by Watson-Crick base pairing to the sequence of the sense strand. These changes to the sense and anti-sense strand codons relating to the specified gly

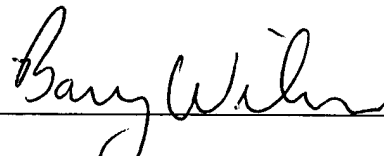
residue of Table X have also been made to the corresponding codons in the Tp1 and Tp4 sequences, respectively, as seen in Table III.

The codon for the C- terminal most phe of the double stranded DNA sequence of Table X has been changed from "ccg" (pro) to "ttt" (phe). Thus, the codon ccg has been changed to ttt to properly encode the indicated amino acid phenylalanine (phe). Support for the C-terminal most phe in Table X is found in the specification at page 37, paragraph [0115] (citing to Suemeri et al., PNAS 88:11017-11021, 1991 for the sequence of TpS2) and by Suemeri et al., Fig. 3 (copy previously attached), which shows a phe at the end of the sequence for TpS2. No new matter is implicated by this change as the encoding DNA sequence has been conformed to the amino acid sequence of the table. The anti-sense strand codon that corresponds to this change also has been changed from cgg to aaa. No new matter is added as this change is predicted by Watson-Crick base pairing to the sequence of the sense strand. These changes to the sense and anti-sense strand codons relating to the specified phe residue of Table X have also been made to the corresponding codons in the Tp3 and Tp6 sequences, respectively, as seen in Table III.

The new Sequence Listing paper copy and computer disk reflect the sequence changes discussed above. Thus, the amendments to the specification raise no issue of new matter.

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